RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/501, 098_

Source: _IFWO_

Date Processed by STIC: _06/24/2005_

ENTERED

IFWO

```
 3 <110> APPLICANT: Petzelt, Christian
 5 <120> TITLE OF INVENTION: Cytotoxic Cyplasin of the Sea Hare, Aplysia Punctata, cDNA
 7 <130> FILE REFERENCE: 4121-169
 9 <140> CURRENT APPLICATION NUMBER: 10/501,098
C--> 10 <141> CURRENT FILING DATE: 2004-07-07
12 <150> PRIOR APPLICATION NUMBER: PCT/EP02/14511
13 <151> PRIOR FILING DATE: 2002-12-18
15 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 558
21 <212> TYPE: PRT
22 <213> ORGANISM: Aplysia punctata
24 <400> SEQUENCE: 1
26 Met Ala Val Arg Phe Leu Ala Pro Gly Leu Leu Thr Leu Ala Thr Leu
27 1               5                  10                  15
30 Val Ser Gly Arg Thr Val Cys Glu Ser Lys Gln Glu Cys Asp Ala Ala
31              20                  25                  30
34 Gln Cys Asp Lys Thr Leu Asp Val Ala Ile Val Gly Ala Gly Ala Ala
35              35                  40                  45
38 Gly Ala Tyr Ser Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly
39      50                  55                  60
42 Val Phe Glu Phe Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln
43 65                  70                  75                  80
46 Leu Pro Asn Thr Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr
47              85                  90                  95
50 Ile Thr Gly Ala His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly
51              100                 105                 110
54 Leu Thr Pro Val Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr
55              115                 120                 125
58 Arg Tyr Tyr Leu Arg Gly Gln Ser Leu Thr Phe Gln Glu Val Leu Thr
59      130                 135                 140
62 Gly Asp Val Pro Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp
63 145                 150                 155                 160
66 Asn Ile Phe Ala Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly
67              165                 170                 175
70 Asp Gly Phe Val Thr Arg Glu Gln Leu Leu Lys Leu Arg Val Ser Asp
71              180                 185                 190
74 Gly Arg Leu Leu Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val
75      195                 200                 205
78 Ala Ser Pro Glu Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr
79      210                 215                 220
82 Thr Glu Val Ser Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His
```

```
83  225                    230               235                    240
86  Leu Gly Glu Asp Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly
87                    245                250                    255
90  Met Gln Lys Val Pro Glu Gln Leu Leu Arg Ala Phe Gly Asn Ser Ser
91                260                265                270
94  Val Phe Gly His Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg
95            275                280                285
98  Ser Lys Ser Asp Lys Ser His Val Leu Tyr Phe Arg Thr Thr Ser Thr
99        290                295                300
102 Val Asp Gly Lys Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val
103 305                310                315                    320
106 Cys Thr Arg Gln Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln
107                325                330                335
110 Val Asp Trp Pro Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly
111           340                345                350
114 Ala Val Arg Thr Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln
115           355                360                365
118 Pro Trp Trp Leu Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr
119       370                375                380
122 Lys Gly Asp Thr Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Ser Glu
123 385                390                395                    400
126 Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Asn Asn
127                405                410                415
130 Thr Leu Phe Gln Arg Val Leu Arg Asp Gln Gly Glu Pro Ile Asn Gly
131           420                425                430
134 Ser Glu Ala Gly Ala His Ile Val Ser Glu Pro Leu Lys Asn Gln Ile
135           435                440                445
138 Leu Asp His Leu Ala Asp Ala Phe Gly Val Pro Arg Ser Asp Ile Gln
139       450                455                460
142 Glu Pro Lys Thr Ala Val Ser Lys Phe Trp Thr Asp Tyr Pro Phe Gly
143 465                470                475                    480
146 Cys Gly Trp Ile Thr Trp Arg Ala Gly Tyr His Phe Asp Asp Val Met
147                485                490                495
150 Asn Thr Met Arg Arg Pro Ser Leu Thr Asp Glu Val Tyr Val Val Gly
151           500                505                510
154 Ala Asp Tyr Ser Trp Gly Leu Ile Ser Ser Trp Val Glu Gly Ala Leu
155           515                520                525
158 Glu Thr Ser Tyr Glu Val Ile Asp Thr Tyr Phe Lys Ser Glu Arg Ser
159       530                535                540
162 His Asn Val Gln Pro Pro Ser His Met Ala Ser His Val Gly
163 545                550                555
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 421
168 <212> TYPE: PRT
169 <213> ORGANISM: Aplysia punctata
171 <400> SEQUENCE: 2
173 Met Ala Val Arg Phe Leu Ala Pro Gly Leu Leu Thr Leu Ala Thr Leu
174 1               5                10                15
177 Val Ser Gly Arg Thr Val Cys Glu Ser Lys Gln Glu Cys Asp Ala Ala
```

RAW SEQUENCE LISTING   DATE: 06/24/2005
PATENT APPLICATION: US/10/501,098   TIME: 11:27:04

Input Set : A:\4121-169.ST25.txt
Output Set: N:\CRF4\06242005\J501098.raw

```
178            20              25              30
181 Gln Cys Asp Lys Thr Leu Asp Val Ala Ile Val Gly Ala Gly Ala Ala
182         35              40              45
185 Gly Ala Tyr Ser Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly
186     50              55              60
189 Val Phe Glu Phe Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln
190 65              70              75              80
193 Leu Pro Asn Thr Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr
194             85              90              95
197 Ile Thr Gly Ala His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly
198         100             105             110
201 Leu Thr Pro Val Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr
202     115             120             125
205 Arg Tyr Tyr Pro Arg Gly Gln Ser Leu Thr Phe Gln Glu Ala Leu Thr
206     130             135             140
209 Gly Asp Val Pro Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp
210 145             150             155             160
213 Asn Ile Phe Ala Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly
214             165             170             175
217 Asp Gly Phe Val Thr Arg Glu Gln Leu Leu Lys Leu Arg Ala Ser Asp
218         180             185             190
221 Gly Arg Pro Leu Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val
222     195             200             205
225 Ala Ser Pro Glu Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr
226     210             215             220
229 Thr Glu Val Ser Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His
230 225             230             235             240
233 Leu Gly Glu Asp Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly
234             245             250             255
237 Met Gln Lys Val Pro Glu Gln Pro Leu Arg Ala Phe Gly Asn Ser Ser
238         260             265             270
241 Val Phe Gly His Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg
242     275             280             285
245 Ala Lys Ser Asp Lys Ser His Val Pro Tyr Phe Arg Pro Thr Ser Thr
246     290             295             300
249 Val Asp Gly Lys Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val
250 305             310             315             320
253 Cys Ala Arg Gln Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln
254             325             330             335
257 Val Asp Trp Pro Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly
258         340             345             350
261 Ala Val Arg Thr Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln
262     355             360             365
265 Pro Trp Trp Leu Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr
266     370             375             380
269 Lys Gly Asp Thr Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Pro Asn
270 385             390             395             400
273 Val Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Ser Thr
274             405             410             415
```

Input Set : A:\4121-169.ST25.txt
Output Set: N:\CRF4\06242005\J501098.raw

```
277 Gln Pro Trp Ile His
278             420
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 506
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Synthetic Construct
289 <400> SEQUENCE: 3
291 Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly Val Phe Glu Phe
292 1               5                   10                  15
295 Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn Thr
296             20                  25                  30
299 Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr Ile Thr Gly Ala
300             35                  40                  45
303 His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly Leu Thr Pro Val
304     50                  55                  60
307 Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr Arg Tyr Tyr Leu
308 65                  70                  75                  80
311 Arg Gly Gln Ser Leu Thr Phe Gln Glu Val Leu Thr Gly Asp Val Pro
312             85                  90                  95
315 Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp Asn Ile Phe Ala
316             100                 105                 110
319 Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly Asp Gly Phe Val
320             115                 120                 125
323 Thr Arg Glu Gln Leu Leu Lys Leu Arg Val Ser Asp Gly Arg Leu Leu
324     130                 135                 140
327 Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val Ala Ser Pro Glu
328 145                 150                 155                 160
331 Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr Thr Glu Val Ser
332             165                 170                 175
335 Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His Leu Gly Glu Asp
336             180                 185                 190
339 Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly Met Gln Lys Val
340             195                 200                 205
343 Pro Glu Gln Leu Leu Arg Ala Phe Gly Asn Ser Ser Val Phe Gly His
344     210                 215                 220
347 Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg Ser Lys Ser Asp
348 225                 230                 235                 240
351 Lys Ser His Val Leu Tyr Phe Arg Thr Thr Ser Thr Val Asp Gly Lys
352             245                 250                 255
355 Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val Cys Thr Arg Gln
356             260                 265                 270
359 Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln Val Asp Trp Pro
360             275                 280                 285
363 Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly Ala Val Arg Thr
364     290                 295                 300
367 Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
368 305                 310                 315                 320
```

RAW SEQUENCE LISTING   DATE: 06/24/2005
PATENT APPLICATION: US/10/501,098   TIME: 11:27:04

Input Set : A:\4121-169.ST25.txt
Output Set: N:\CRF4\06242005\J501098.raw

```
371 Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr Lys Gly Asp Thr
372             325                 330                 335
375 Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Ser Glu Ala Ser Gly Asp
376             340                 345                 350
379 Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Asn Asn Thr Leu Phe Gln
380             355                 360                 365
383 Arg Val Leu Arg Asp Gln Gly Glu Pro Ile Asn Gly Ser Glu Ala Gly
384     370                 375                 380
387 Ala His Ile Val Ser Glu Pro Leu Lys Asn Gln Ile Leu Asp His Leu
388 385                 390                 395                 400
391 Ala Asp Ala Phe Gly Val Pro Arg Ser Asp Ile Gln Glu Pro Lys Thr
392             405                 410                 415
395 Ala Val Ser Lys Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile
396             420                 425                 430
399 Thr Trp Arg Ala Gly Tyr His Phe Asp Asp Val Met Asn Thr Met Arg
400             435                 440                 445
403 Arg Pro Ser Leu Thr Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser
404     450                 455                 460
407 Trp Gly Leu Ile Ser Ser Trp Val Glu Gly Ala Leu Glu Thr Ser Tyr
408 465                 470                 475                 480
411 Glu Val Ile Asp Thr Tyr Phe Lys Ser Glu Arg Ser His Asn Val Gln
412             485                 490                 495
415 Pro Pro Ser His Met Ala Ser His Val Gly
416             500                 505
419 <210> SEQ ID NO: 4
420 <211> LENGTH: 12
421 <212> TYPE: PRT
422 <213> ORGANISM: Artificial Sequence
424 <220> FEATURE:
425 <223> OTHER INFORMATION: Synthetic construct
427 <400> SEQUENCE: 4
429 Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp
430 1               5                   10
433 <210> SEQ ID NO: 5
434 <211> LENGTH: 1518
435 <212> TYPE: DNA
436 <213> ORGANISM: Aplysia punctata
438 <400> SEQUENCE: 5
439 gcctaccttt tgaggaataa aggtcagaac atcggggtct tcgaattctg tgacagagtg      60
441 ggtggtcggc tgttcaccta tcagttgcct aatacccccg acgtgcagct ggaactgggc     120
443 gggatgcggt acatcaccgg cgctcataac ctgctcgagg gagtcgttcg tcagctggga     180
445 ctgaccccag tagtgtttac agaaggcttc ggtaagctgg ccgtacacg ctattacctg      240
447 aggggacagt ccctgacctt ccaggaagtg ctgacaggcg acgtgccata caaccttacc     300
449 gtcgcggaga agcagaacca ggacaatatt ttcgccttct atctcaagga actaacccgt     360
451 ttcgacgtag gcgacggttt cgtgaccaga gaacaactgc tgaaactgcg cgtcagcgat     420
453 gggaggctcc tctaccaact gacgttcgac gaagccctgg acctggtagc atcgccggaa     480
455 ggtaaagaat ttgccaggga cattcacgtg tttacgacgg aggtttcaga cgacgccaac     540
457 gcggtttcgg tgttcgacga cgacttaggt gaggacggcg taggcgagga gatccatacc     600
459 gtgcaagaag gaatgcagaa agtaccggag caactgctgc gtgcatttgg aaacagttcc     660
```

VERIFICATION SUMMARY   DATE: 06/24/2005
PATENT APPLICATION: US/10/501,098   TIME: 11:27:05

Input Set : A:\4121-169.ST25.txt
Output Set: N:\CRF4\06242005\J501098.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date